

CC gene, the mammary gland response element of the beta-casein gene
CC and a SV40 immediate element at the PstAI gene.
XX Sequence 100 BP: 26 A: 17 C: 33 G: 24 T: 0 other:
SQ Query Match 85.7% Score 16: 18 24: Length 100:
XX Best Local Similarity 100.0%
XX Matches 18: Conservative 0 Mismatches 0 Indels 0 Gaps 0
CY 1 AGATTTCAGCATTCGA 18
DB 38 AGATTTCAGCATTCGA 21
|||||

RESUME 6
ID: ABA93801 standard; NM: 100 BP.
XX ABA93801.
XX 01-MAY-2002 (first entry)
XX K213A plasmid construction oligonucleotide SEQ ID NO:43.
XX Zcytor17, chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX immunoregulatory; antiviral; antineoplastic; antitumor; cytostatic;
XX muscular; lymphoid; immune; inflammatory; leukocyte; Crohn's disease;
XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX inflammatory disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX inflammatory disease; pericarditis; inflammatory bowel disease;
XX PCR primer; probe; ss.
XX Synthetic.
XX WC20020721-42.
XX 03-JAN-2002.
XX 26-JUN-2001; 2001HO-0520484.
XX 26-JUN-2001; 2000US-2142829.
XX 26-JUN-2001; 2000US-2142829.
XX 08-FEB-2001; 2000US-287933F.
XX (Zymo) ZYMOGENETICS INC.
XX Sprecher CA, Frenkel SH, Gao Z, Whitmore TE, Kulper JI.
XX Nature NY.
XX WFI: 2002-090519/12.
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
XX useful for treating and diagnosing lymphoid, immune, inflammatory,
XX splenic, blood or bone disorders.
XX Example 19: Page 190: 235pp: English.
XX The present invention describes a cytokine receptor designated zcytor17.
XX zcytor17 has immunomodulatory, antiviral, antineoplastic, cytostatic,
XX antitumor, antileukemic and muscular activities. The zcytor17
XX proteins are useful for treating and diagnosing lymphoid, immune,
XX anti-zcytor17 antibodies are useful in stimulating or repressed
XX immunity and for stimulating lymphocyte proliferation, such as in the
XX viral infections. They are also useful in the treatment of certain
XX for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX sclerosis) and inflammatory bowel disease. zcytor17 can cancer,
XX chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX exemplification of the present invention.

XX Sequence 100 BP: 24 A: 33 C: 17 G: 26 T: 0 other:
SQ Query Match 85.7% Score 16: 18 24: Length 100:
XX Best Local Similarity 100.0%
XX Matches 18: Conservative 0 Mismatches 0 Indels 0 Gaps 0
CY 1 AGATTTCAGCATTCGA 18
DB 67 AGATTTCAGCATTCGA 84
|||||

RESUME 7
ID: ABA93802 standard; NM: 100 BP.
XX ABA93802.
XX 01-MAY-2002 (first entry)
XX K213A plasmid construction oligonucleotide SEQ ID NO:44.
XX Zcytor17, chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX immunoregulatory; antiviral; antineoplastic; antitumor; cytostatic;
XX muscular; lymphoid; immune; inflammatory; leukocyte; Crohn's disease;
XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX inflammatory disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX inflammatory disease; pericarditis; inflammatory bowel disease;
XX PCR primer; probe; ss.
XX Synthetic.
XX WC20020721-42.
XX 03-JAN-2002.
XX 26-JUN-2001; 2001HO-0520484.
XX 26-JUN-2001; 2000US-2142829.
XX 26-JUN-2001; 2000US-2142829.
XX 08-FEB-2001; 2000US-287933F.
XX (Zymo) ZYMOGENETICS INC.
XX Sprecher CA, Frenkel SH, Gao Z, Whitmore TE, Kulper JI.
XX Nature NY.
XX WFI: 2002-090519/12.
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
XX useful for treating and diagnosing lymphoid, immune, inflammatory,
XX splenic, blood or bone disorders.
XX Example 19: Page 190: 235pp: English.
XX The present invention describes a cytokine receptor designated zcytor17.
XX zcytor17 has immunomodulatory, antiviral, antineoplastic, cytostatic,
XX antitumor, antileukemic and muscular activities. The zcytor17
XX proteins are useful for treating and diagnosing lymphoid, immune,
XX anti-zcytor17 antibodies are useful in stimulating or repressed
XX immunity and for stimulating lymphocyte proliferation, such as in the
XX viral infections. They are also useful in the treatment of certain
XX for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX sclerosis) and inflammatory bowel disease. zcytor17 can cancer,
XX chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX exemplification of the present invention.

DB 38 ADATTTCAGCATTTCA 21

RESULT 10

AD022954 standard; DNM, 100 BP.

AD022954:

26-FEB-2002 (first entry)

Baf3/K134/zalpa1 cell line constructing K12/748 oligonucleotide.

XX zalpa11: cytokine receptor; immunosuppressive; cytotoxic; infectious;
 XX anti-leukemia; cancer; proinflammatory; systemic lupus erythematosus;
 XX rheumatoid arthritis;
 XX diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
 XX inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
 XX asthma; se.

XX Unidentified.

XX W020017171-42.

XX 18-OCT-2001.

XX 03-APR-2001: 2001MO-0510872.

XX 05-APR-2000: 2000US-184731P.

XX 28-JUL-2000: 2000US-221212P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Novak JE, West JW, Pressnell SR, Holly RD, Nelson AJ.

XX WPI: 2002-025899/03.

XX Novel soluble receptor polypeptides and polynucleotides used as
 XX proliferation of hematopoietic cells and for suppressing immune
 XX response in a mammal.

XX Example 19: Page 213: 243pp. Eng1187.

XX The invention relates to an isolated soluble zalpa11 cytokine receptor
 XX polypeptide and their complementary nucleic acids, and methods for
 XX inhibiting or antagonizing the ligand activity-induced proliferation of
 XX hematopoietic cells and hematopoietic cell progenitors preferably
 XX lymphoid cells which are of natural killer cells or cytotoxic T cells.
 XX zalpa11 is useful for treating immune and inflammatory disorders, for
 XX reducing proliferation of neoplastic B or T cells, for suppressing an
 XX immune response in a mammal exposed to an antigen or pathogen, including
 XX cancer, for treating autoimmune disease such as rheumatoid arthritis, multiple sclerosis,
 XX systemic lupus erythematosus (SLE) and diabetes;
 XX myasthenia gravis; systemic lupus erythematosus (SLE) and diabetes;
 XX myasthenia gravis; systemic lupus erythematosus (SLE) and diabetes;
 XX sepsis, viral infection (dengue virus infection) and cancer. The present
 XX sequence is an oligonucleotide used for Baf3/K134/zalpa11 cell line
 XX construction.

XX Sequence 100 BP: 24 A: 33 C: 17 G: 26 T: 0 other:

XX Query Match 85.7% Score 18: 88 24: Length 100:

XX Best Local Similarity 100.00: Pctd No. 63:

XX Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

XX 1 AGATTTCAGCATTTCA 18

XX DB 67 ADATTTCAGCATTTCA 84

RESULT 11

AD022954/C

AD022954 standard; DNM, 100 BP.

AD022954:

26-FEB-2002 (first entry)

Baf3/K134/zalpa1 cell line constructing K12/748 oligonucleotide.

XX zalpa111: cytokine receptor; immunosuppressive; cytotoxic; hematocytic;
 XX inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
 XX systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
 XX diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
 XX inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
 XX asthma; se.

XX Unidentified.

XX W020017171-42.

XX 18-OCT-2001.

XX 03-APR-2001: 2001MO-0510872.

XX 05-APR-2000: 2000US-184731P.

XX 28-JUL-2000: 2000US-221212P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Novak JE, West JW, Pressnell SR, Holly RD, Nelson AJ.

XX WPI: 2002-025899/03.

XX Novel soluble receptor polypeptides and polynucleotides used as
 XX proliferation of hematopoietic cells and for suppressing immune
 XX response in a mammal.

XX Example 19: Page 213: 243pp. Eng1187.

XX The invention relates to an isolated soluble zalpa11 cytokine receptor
 XX polypeptide and their complementary nucleic acids, and methods for
 XX inhibiting or antagonizing the ligand activity-induced proliferation of
 XX hematopoietic cells and hematopoietic cell progenitors preferably
 XX lymphoid cells which are of natural killer cells or cytotoxic T cells.
 XX zalpa11 is useful for treating immune and inflammatory disorders, for
 XX reducing proliferation of neoplastic B or T cells, for suppressing an
 XX immune response in a mammal exposed to an antigen or pathogen, including
 XX cancer, for treating autoimmune disease such as rheumatoid arthritis, multiple sclerosis,
 XX systemic lupus erythematosus (SLE) and diabetes;
 XX myasthenia gravis; systemic lupus erythematosus (SLE) and diabetes;
 XX myasthenia gravis; systemic lupus erythematosus (SLE) and diabetes;
 XX sepsis, viral infection (dengue virus infection) and cancer. The present
 XX sequence is an oligonucleotide used for Baf3/K134/zalpa11 cell line
 XX construction.

XX Sequence 100 BP: 26 A: 17 C: 33 G: 24 T: 0 other:

XX Query Match 85.7% Score 18: 88 24: Length 100:

XX Best Local Similarity 100.00: Pctd No. 63:

XX Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

XX 1 AGATTTCAGCATTTCA 18

XX DB 38 ADATTTCAGCATTTCA 21

RESULT 12

ABR88204/C

ABR88204 standard; DNM, 33 BP.

ABR88204:

ABR88204:

07-OCT-2002 (first entry)
 Human cytochrome bcl core protein cDNA specific PCR primer 12.
 Cytochrome bcl; primer: ss; core protein 1112, 21; cancer; HIV;
 human immunodeficiency virus; human; PCR.
 Homo sapiens.
 CN140524-A.
 20-MAR-2002.
 31-MAR-2000; 2000CN-0119831.
 31-MAR-2000; 2000CN-0119831.
 (RBOE-) BODE GENE DEV CO LTD SHANGHAI
 Mo Y, Xie Y;
 WPI: 2001-4361847.
 poly(epsilon)-human cytochrome bcl compound core protein 11.12.21 and
 poly(epsilon)-bcl for coding 11-21.
 Example 4: Page 19 (disclosure); 34pp; Glaxo.
 This invention relates to the cDNA and protein sequences of a novel
 poly(epsilon)-human cytochrome bcl compound core protein 1112, 21. The
 poly(epsilon)-human cytochrome bcl compound core protein 1112, 21. The
 recombinant DNA technology and a method for the application of the
 poly(epsilon)-human cytochrome bcl compound core protein 1112, 21.
 poly(epsilon)-human cytochrome bcl compound core protein 1112, 21.
 Its therapeutic action, and the application of the poly(epsilon)-human
 cytochrome bcl compound core protein 1112, 21 cDNA of the invention.
 Sequence 33 BP; 10 A; 10 C; 4 G; 9 T; 0 other;
 Query Match: 76.2%; Score 16; DB 24; Length 33;
 Best Local Similarity: 100.0%; Pred. No. 5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AATTTCGAGATTC 16
 19 NAAATTGAGATTC 4
 RESULT 13
 AAL1509
 ID AAL1509 standard; DNM: 51 BP.
 AC AAL1509;
 24-JAN-2002 (first entry)
 Human SNP oligonucleotide 44817.
 Immunoprecipitation; immunofluorescence; cytochrome
 neuroprotective; angiotensin; apoptosis related protein; cancer;
 angiotensin; angiotensin; angiotensin; angiotensin; angiotensin;
 complement related protein; kinase; cytokine stimulating factor;
 interleukin; G-protein coupled receptor; cholesteryl; inflammation;
 multicystic disease; autoimmune disease; infection;
 nervous system disease; as;
 Homo sapiens.
 W020017944-A2.

05-JUL-2001.
 28-DEC-2000; 2000CN-0834498.
 28-DEC-1999; 99US-0173410
 27-DEC-2000; 2000US-0173419.
 (CDNA-) CDNA GEN COMP.
 Shinkens RA, Leach M;
 WPI: 2001-465210/50.
 poly(epsilon) nucleic acids encoding e.g. amyases, cyclins, polymerases,
 cancer; autoimmune disease and infection.
 Claim 1: Page 273; 413pp; English.
 The present invention relates to oligonucleotides encoding polymorphic
 variants of proteins related to amyases, angiotensin, angiotensin,
 histones, kinases, colon stimulating factors, complement related,
 proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 one such oligonucleotide is an oligonucleotide. The present sequence 13
 by them may be used in the prevention, diagnosis and treatment of
 diseases associated with inappropriate expression of the proteins listed
 diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 leukemia), diseases of the nervous system and an infection of pathogenic
 organisms.
 Sequence 51 BP; 42 A; 6 C; 8 G; 15 T; 0 other;
 Query Match: 73.3%; Score 15; 4; DB 22; Length 51;
 Best Local Similarity: 94.1%; Pred. No. 9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 3 AATTTCGAGATTC 19
 9 AATTTCGAGATTC 25
 RESULT 14
 AAL1509/C
 ID AAL1509 standard; DNM: 41 BP.
 AC AAL1509;
 29-MAR-2002 (first entry)
 Oligonucleotide 325.
 Y-triester; vaccine; foot and mouth disease; P1 region; capsid;
 JC provirus; as;
 Foot and mouth disease virus.
 JC provirus; as;
 03-JAN-2002.
 27-JUN-2001; 2001MO-F00447.
 29-JUN-2001; 2001PR-0008437.
 (MER-) MERIAL.
 King A, Burman A, Anderson J, Lombard M;

XX WPI: 2002-130837/7.

XX Stable, potent effective vaccine against foot-and-mouth disease.
XX completes recombinantly produced empty virus capsids as antigens.

XX Example 7, Page 29: 79pp; French.

XX The present invention relates to a vaccine against foot and mouth disease
XX (FMD) comprising (in addition to a veterinary vehicle excipient) an
XX antigen consisting of the empty FMD virus capsids, obtained by expression in
XX eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX the P1 region encoding the capsid and the region encoding the 3C protease;
XX at low doses. The vaccine is useful against foot and mouth disease/
XX especially in cows, sheep, pigs or goats. The present sequence is an
XX oligonucleotide which was used in an example from the invention.

XX Sequence 41 BP; 13 A; 7 C; 6 G; 15 T; 0 other;

XX Query Match: 70.5%; Score 14.8; DN 24; Length 41;

XX Best Local Similarity: 88.9%; Prob. No. 1.8e-03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2 GATTTCGGAATTCGAA 19
XX 19 GATTTCGGAATTCGAA 2

XX RESULT 15

XX ID AB153041 standard: DN; 4; BP.

XX AB153041:

XX 29-MAY-2002 (first entry)

XX Oligonucleotide JCA 127.

XX Virulence: vaccine; foot and mouth disease; P1 region; capsid;

XX 3C protease; 69.

XX Foot and mouth disease virus.

XX WC00000251-A1.

XX 03-MAY-2002.

XX 27-JUN-2001: 2001MO-FR0240.

XX 29-JUN-2000: 2000FR-0008437.

XX (MER-) MERIAL.

XX King A. Bureau A. Audomercet J. Lombard M:

XX WPI: 2002-130837/17.

XX Stable, potent effective vaccines against foot-and-mouth disease.
XX completes recombinantly produced empty virus capsids as antigens.

XX Example 7, Page 30: 79pp; French.

XX The present invention relates to a vaccine against foot and mouth disease
XX (FMD) comprising (in addition to a veterinary vehicle or excipient) an
XX antigen consisting of the empty FMD virus capsids, obtained by expression in
XX eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX the P1 region encoding the capsid and the region encoding the 3C protease;
XX at low doses. The vaccine is useful against foot and mouth disease,
XX especially in cows, sheep, pigs or goats. The present sequence is an
XX oligonucleotide which was used in an example from the invention.

XX Sequence 41 BP; 13 A; 6 C; 6 G; 15 T; 0 other;

XX Query Match: 70.5%; Score 14.8; DN 24; Length 41;

XX Best Local Similarity: 88.9%; Prob. No. 1.8e-03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 2 GATTTCGGAATTCGAA 19
XX 19 GATTTCGGAATTCGAA 2

XX Search completed: December 25, 2002, 12:55:32
XX Job time: 1375 secs

GenScore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: December 25, 2002, 12:59:50 ; Search time 2664 seconds
(without alignments)

97,588 Million cell updates/sec

Title: SCMD1675

Perfect score: 9

Sequence: 1 kcmgann 9

Scoring table: IDENTITY_NIC

Gap: 10.0, Gapex: 1.0

Search: 205460 seqs, 1455102878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 04

Listing file: 43 summaries

Database : GenBank
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2: gb-acc*
3: gb-acc*
4: gb-acc*
5: gb-acc*
6: gb-acc*
7: gb-acc*
8: gb-acc*
9: gb-acc*
10: gb-acc*
11: gb-acc*
12: gb-acc*
13: gb-acc*
14: gb-acc*
15: gb-acc*
16: gb-acc*
17: gb-acc*
18: gb-acc*
19: gb-acc*
20: gb-acc*
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25: gb-acc*
26: gb-acc*
27: gb-acc*
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35: gb-acc*
36: gb-acc*
37: gb-acc*
38: gb-acc*
39: gb-acc*
40: gb-acc*
41: gb-acc*
42: gb-acc*
43: gb-acc*
44: gb-acc*
45: gb-acc*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB ID	Description
1	66.7	9	6	AX041991	AX041991 Sequence
2	66.7	9	6	AX041991	AX041991 Sequence
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4	66.7	9	6	AX041991	AX041991 Sequence
5	66.7	9	6	AX041991	AX041991 Sequence
6	66.7	9	6	AX041991	AX041991 Sequence
7	66.7	9	6	AX041991	AX041991 Sequence
8	66.7	9	6	AX041991	AX041991 Sequence
9	66.7	9	6	AX041991	AX041991 Sequence
10	66.7	9	6	AX041991	AX041991 Sequence
11	66.7	9	6	AX041991	AX041991 Sequence
12	66.7	9	6	AX041991	AX041991 Sequence
13	66.7	9	6	AX041991	AX041991 Sequence
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27	66.7	9	6	AX041991	AX041991 Sequence
28	66.7	9	6	AX041991	AX041991 Sequence
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31	66.7	9	6	AX041991	AX041991 Sequence
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33	66.7	9	6	AX041991	AX041991 Sequence
34	66.7	9	6	AX041991	AX041991 Sequence
35	66.7	9	6	AX041991	AX041991 Sequence
36	66.7	9	6	AX041991	AX041991 Sequence
37	66.7	9	6	AX041991	AX041991 Sequence
38	66.7	9	6	AX041991	AX041991 Sequence
39	66.7	9	6	AX041991	AX041991 Sequence
40	66.7	9	6	AX041991	AX041991 Sequence
41	66.7	9	6	AX041991	AX041991 Sequence
42	66.7	9	6	AX041991	AX041991 Sequence
43	66.7	9	6	AX041991	AX041991 Sequence
44	66.7	9	6	AX041991	AX041991 Sequence
45	66.7	9	6	AX041991	AX041991 Sequence

ALIGNMENTS



RESULT 1
LOCUS AX041991
VERSION AX041991.1
SOURCE human
ORGANISM Homo sapiens
REFERENCE Nelson, S., Wood, L., and Lin, B.
TITLE Specific polynucleotides, polypeptides and their methods

Print. No. is the number of results predicted by chance to have a

Db 2 TTCOMCAG 10

RESULT 10
 AXX01563/0
 DEFINITION Sequence 53 from patent US 5814517.
 ACCESSION AXX01563.1 GI:594691
 VERSION
 JOURNAL
 FEATURES

Db 1 TTCOMCAG 9

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Seldin, J. Martin, and Lamb, J. Peter.
 TITLE The spacer-regulatory elements responsive to cytokines and methods
 for their use.
 JOURNAL Patent: US 5814517-A 53 29-SEP-1998
 FEATURES Location/Qualifiers
 source
 /organism="homo sapiens"

BASE COUNT 4 a 1 c 1 g 4 t
 ORIGIN

Query Match 66.7%; Score 6; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2,3e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 TTCOMCAG 9
 Db 10 TTCOMCAG 2

RESULT 11
 AXX01514
 DEFINITION Sequence 228 from Patent WO0185941.
 ACCESSION AXX01514.1 GI:1738297
 VERSION
 JOURNAL
 FEATURES

Db 1 TTCOMCAG 9

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Versteeg, R. and Carton, H. N.
 TITLE The human interleukin-10 gene.
 JOURNAL Academic Press, Amsterdam, 1998.
 FEATURES Location/Qualifiers
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 /organism="homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2 a 1 c 2 g 5 t
 ORIGIN

Query Match 66.7%; Score 6; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2,3e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 TTCOMCAG 9
 Db 1 TTCOMCAG 9

RESULT 12
 AXX01514/0
 DEFINITION Sequence 228 from Patent WO0185941.
 ACCESSION AXX01514.1 GI:1738297
 VERSION
 JOURNAL
 FEATURES

Db 1 TTCOMCAG 9

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Versteeg, R. and Carton, H. N.
 TITLE The human interleukin-10 gene.
 JOURNAL Academic Press, Amsterdam, 1998.
 FEATURES Location/Qualifiers
 source
 /organism="homo sapiens"
 /db_xref="taxon:9606"

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Versteeg, R. and Carton, H. N.
 TITLE The human interleukin-10 gene.
 JOURNAL Academic Press, Amsterdam, 1998.
 FEATURES Location/Qualifiers
 source
 /organism="homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2 a 1 c 2 g 5 t
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Query Match 66.7%; Score 6; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2,3e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 13
 AXX01563
 DEFINITION Sequence 277 from Patent WO0185941.
 ACCESSION AXX01563
 VERSION
 JOURNAL
 FEATURES

Db 1 TTCOMCAG 9

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Versteeg, R. and Carton, H. N.
 TITLE The human interleukin-10 gene.
 JOURNAL Academic Press, Amsterdam, 1998.
 FEATURES Location/Qualifiers
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 /organism="homo sapiens"
 /db_xref="taxon:9606"

Db 1 TTCOMCAG 9

BASE COUNT 2 a 1 c 2 g 5 t
 ORIGIN

Query Match 66.7%; Score 6; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2,3e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 TTCOMCAG 9
 Db 1 TTCOMCAG 9

RESULT 14
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 DEFINITION Sequence 277 from Patent WO0185941.
 ACCESSION AXX01563.1 GI:1738246
 VERSION
 JOURNAL
 FEATURES

Db 1 TTCOMCAG 9

ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Versteeg, R. and Carton, H. N.
 TITLE The human interleukin-10 gene.
 JOURNAL Academic Press, Amsterdam, 1998.
 FEATURES Location/Qualifiers
 source
 /organism="homo sapiens"
 /db_xref="taxon:9606"

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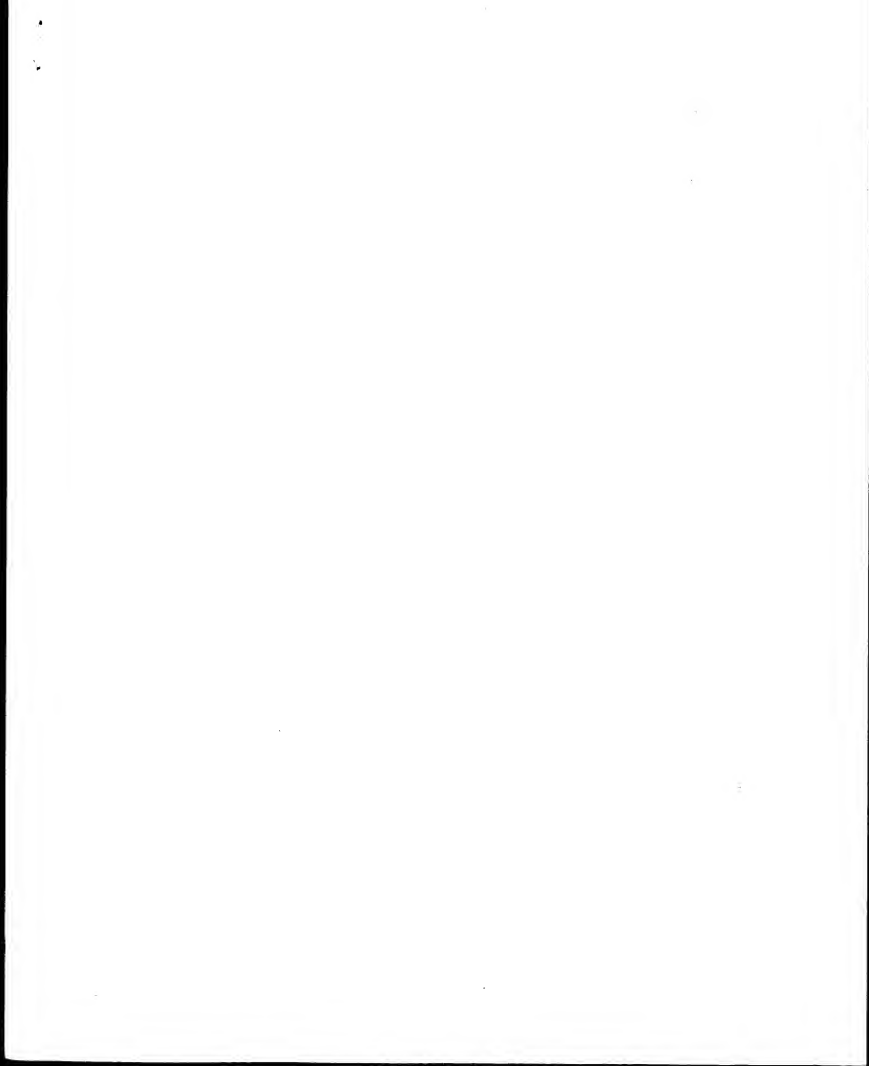
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Query Match     66.7%: Score 6; 1a 6; Length 10;
                best local similarity 66.7%; 1a 6; 2a+06;
Matches 0; conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 TTCTGGGA 9
    1 11 11 11
Db 9 TTCTGGGA 1

RESULT 15
A92561          11 bp      DNA      linear    PAT 22-JAN-2000
LOCUS          A92561
DEFINITION     Sequence 2 from Patent WO9812120.
ACCESSION      A92561
VERSION        A92561.1 GI:6741220
KEYWORDS
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1. Stocklin B and Kromer A
               (1998) NUCLEIC ACID CONSTRUCT/SCORING FOR A PROTEIN COMPLEX FROM A STAT
               PROTEIN AND NUCLEIC ACID RECEPTOR AND ITS USE
               IN PATENT WO 9812120 (1998) 12/12/98
JOURNAL        STOCKLIN B, KROMER A (1998) GENE 218:145-149

FEATURES
Source
Location/Qualifiers
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                best local similarity 66.7%; 1a 6; 2a+06;
Matches 6; conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 TTCTGGGA 9
    1 11 11 11
Db 3 TTCTGGGA 11

Search completed: December 25, 2002, 22:44:35
Job time : 2685 secs

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GenCode version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: December 25, 2002 11:24:49 / Search time 3803 seconds

(without alignments)
157,030 Million cell updates/sec

Title: US-09-744-875-1

Perfect score: 21

Sequence: 1 gagcttcgagatcattac 21

Scoring table: IDENTITY, JNC

Gapop 10.0 / Gapact 1.0

Searched: 205640 seqs, 145140278 residues

Total number of hits satisfying chosen parameters: 995500

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Genbank

1: gb-ba1*

2: gb-ba1*

3: gb-ba1*

4: gb-ba1*

5: gb-ba1*

6: gb-ba1*

7: gb-ba1*

8: gb-ba1*

9: gb-ba1*

10: gb-ba1*

11: gb-ba1*

12: gb-ba1*

13: gb-ba1*

14: gb-ba1*

15: gb-ba1*

16: gb-ba1*

17: gb-ba1*

18: gb-ba1*

19: gb-ba1*

20: gb-ba1*

21: gb-ba1*

22: gb-ba1*

23: gb-ba1*

24: gb-ba1*

25: gb-ba1*

26: gb-ba1*

27: gb-ba1*

28: gb-ba1*

29: gb-ba1*

30: gb-ba1*

31: gb-ba1*

32: gb-ba1*

33: gb-ba1*

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38: gb-ba1*

39: gb-ba1*

40: gb-ba1*

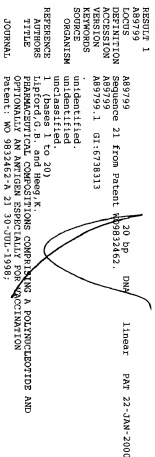
41: gb-ba1*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	18	85.7	20	AB9886	AB9886 Sequence 21
3	18	85.7	20	AB9886	AB9886 Sequence 21
4	18	85.7	20	AB9886	AB9886 Sequence 21
5	18	85.7	100	AB174601	AB174601 Sequence
6	18	85.7	100	AB174602	AB174602 Sequence
7	18	85.7	100	AB174603	AB174603 Sequence
8	18	85.7	100	AB174604	AB174604 Sequence
9	18	85.7	100	AB174605	AB174605 Sequence
10	18	85.7	100	AB174606	AB174606 Sequence
11	18	85.7	100	AB174607	AB174607 Sequence
12	18	85.7	100	AB174608	AB174608 Sequence
13	18	85.7	100	AB174609	AB174609 Sequence
14	18	85.7	100	AB174610	AB174610 Sequence
15	18	85.7	100	AB174611	AB174611 Sequence
16	18	85.7	100	AB174612	AB174612 Sequence
17	18	85.7	100	AB174613	AB174613 Sequence
18	18	85.7	100	AB174614	AB174614 Sequence
19	18	85.7	100	AB174615	AB174615 Sequence
20	18	85.7	100	AB174616	AB174616 Sequence
21	18	85.7	100	AB174617	AB174617 Sequence
22	18	85.7	100	AB174618	AB174618 Sequence
23	18	85.7	100	AB174619	AB174619 Sequence
24	18	85.7	100	AB174620	AB174620 Sequence
25	18	85.7	100	AB174621	AB174621 Sequence
26	18	85.7	100	AB174622	AB174622 Sequence
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ALIGNMENTS



Prod. No. is the number of results predicted by chance to have a

FEATURES LIPROD GRAYSON (DB); HIES KLAUS (DE)

SOURCE Location/Qualifiers

BASE COUNT 7 a 5 c 3 g 7 t

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Best Local Similarity 100.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0;

Db 1 AGATTTCAGAGATCA 18

RESULT 2 A90886 20 bp DNA linear PAT 22-JAN-2000

DEFINITION Sequence 21 from Patent EP0855184.

ACCESSION A90886.1 GI:679328

KEYWORDS unclassified

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 20)

TITLE Phage lambda and lipodot A.B.

AUTHORS Unknown

DATE 08/05/84

ABSTRACT

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

Query Match 85.7% Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0;

Db 1 AGATTTCAGAGATCA 18

RESULT 4 124556 21 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 8 from patent US 554409.

ACCESSION 124556 GI:160326

KEYWORDS unclassified

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 21)

TITLE Cytokine regulated transcription factor

AUTHORS Grover, B., Goulet, X.P. and Haiso, H.

DATE 08/05/84

ABSTRACT

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Query Match 85.7% Score 18; DB 6; Length 100;

Best Local Similarity 100.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0;

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Db 1 AGATTTCAGAGATCA 18

RESULT 6 A8174601 100 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 59 from patent US 6307024.

ACCESSION A8174601 GI:17914921

KEYWORDS unclassified

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 100)

TITLE Cytokine regulated transcription factor

AUTHORS Grover, B., Goulet, X.P. and Haiso, H.

DATE 08/05/84

ABSTRACT

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

Phage lambda and lipodot A.B. are

phages which are capable of associating

with a specific host cell and

releasing a polynucleotide and an

envelope protein.

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 VERSION AB174602.1 GI:1791822
 REMARKS Unknown.
 SOURCE /organism=unknown
 ORGANISM Unknown.
 Unclassified, 100%
 REFERENCE Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
 Gress,A.J., Johnston,J.V., Nelson,A.J., Dillon,S.R., and
 TITLE Cyclin A and Cyclin B1 Lysine
 JOURNAL Patent: US 6,379,244-A 6/25/OCT-2001;
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 ACCESSION AX280202
 VERSION AX280202.1 GI:1187445
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 REFERENCE Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
 AUTHORS Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
 JOURNAL Patent: WO 008381-A 3/18/NOV-2000;
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 BASE COUNT 24 a 33 c 17 g
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 Db 67 AATTTTCAGCATTTCA 84
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 VERSION AX280203.1 GI:1187445
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 SOURCE /db=ncbi/GenBank/RefSeq
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 REFERENCE Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
 AUTHORS Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
 JOURNAL Patent: WO 008381-A 3/18/NOV-2000;
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 Oy 1 AATTTTCAGCATTTCA 18
 Db 38 AATTTTCAGCATTTCA 21

ZymoGenetics, Inc. (US)
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 Db 38 AATTTTCAGCATTTCA 21
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 LOCUS AX280202 48 from Patent WO017171. 100 bp DNA linear PAT 02-NOV-2001
 ACCESSION AX280202
 VERSION AX280202.1 GI:14607595
 REMARKS /organism=synthetic construct
 SOURCE /db=ncbi/GenBank/RefSeq
 ORGANISM synthetic construct
 REFERENCE Sprecher,C.A., Novak,J.E., Moss,D.M., Presnell,S.R., Holly,R.D. and
 AUTHORS Sprecher,C.A., Novak,J.E., Moss,D.M., Presnell,S.R., Holly,R.D. and
 TITLE Cyclin A and Cyclin B1 Lysine
 JOURNAL Patent: WO 017171-A 48 11/OCT-2001;
 FEATURES Location/Qualifiers
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 BASE COUNT 24 a 33 c 17 g
 ORIGIN
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 Matches 18; Conservative 0; Mismatches 0; Indels 0;
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 Db 67 AATTTTCAGCATTTCA 84
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 LOCUS AX280203 49 from Patent WO017171. 100 bp DNA linear PAT 02-NOV-2001
 ACCESSION AX280203
 VERSION AX280203.1 GI:14607596
 REMARKS /organism=synthetic construct
 SOURCE /db=ncbi/GenBank/RefSeq
 ORGANISM synthetic construct
 REFERENCE Sprecher,C.A., Novak,J.E., Moss,D.M., Presnell,S.R., Holly,R.D. and
 AUTHORS Sprecher,C.A., Novak,J.E., Moss,D.M., Presnell,S.R., Holly,R.D. and
 TITLE Cyclin A and Cyclin B1 Lysine
 JOURNAL Patent: WO 017171-A 49 11/OCT-2001;
 FEATURES Location/Qualifiers
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 BASE COUNT 26 a 32 g 25 t
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 Db 67 AATTTTCAGCATTTCA 84

ORIGIN

Query Match 85.7% Score 18; DB 6; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AATTTTCAGATTCATCA 18
 DB 38 AATTTTCAGATTCATCA 21

RESULT 11
 LOCUS AX348191 100 bp DNA Linear PAT 15-FEB-2002
 DEFINITION Sequence 21 from Patent WO0200721.
 ACCESSION AX348191.1 GI:18694947
 VERSION AX348191.1 GI:18694947
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE

Query Match 85.7% Score 18; DB 6; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AATTTTCAGATTCATCA 18
 DB 67 AATTTTCAGATTCATCA 84

RESULT 12
 LOCUS AX365192 100 bp DNA Linear PAT 15-FEB-2002
 DEFINITION Sequence 44 from Patent WO0200721.
 ACCESSION AX365192.1 GI:18694948
 VERSION AX365192.1 GI:18694948
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE

Query Match 85.7% Score 18; DB 6; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 AATTTTCAGATTCATCA 18
 DB 67 AATTTTCAGATTCATCA 84

DB 38 AATTTTCAGATTCATCA 21

RESULT 13
 LOCUS AX348184 100 bp DNA Linear PAT 01-FEB-2002
 DEFINITION Sequence 21 from Patent WO0200721.
 ACCESSION AX348184
 VERSION AX348184.1 GI:18691887
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE

Query Match 70.3% Score 14.8; DB 6; Length 41;
 Best Local Similarity 88.9%; Pred. No. 1.1e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 GATTTTCAGATTCATCA 19
 DB 19 GATTTTCAGATTCATCA 2

RESULT 14
 LOCUS AX348185 41 bp DNA Linear PAT 01-FEB-2002
 DEFINITION Sequence 29 from Patent WO020051.
 ACCESSION AX348185
 VERSION AX348185.1 GI:18691889
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE

Query Match 70.3% Score 14.8; DB 6; Length 41;
 Best Local Similarity 88.9%; Pred. No. 1.1e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 GATTTTCAGATTCATCA 19
 DB 19 GATTTTCAGATTCATCA 2

RESULT 15
 LOCUS AX348182 44 bp DNA Linear PAT 01-FEB-2002
 DEFINITION Sequence 19 from Patent WO0200721.
 ACCESSION AX348182

GenCore version 5.1.3
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OK nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:40:44 ; Search time 22 seconds

Title: SCHMIDT875
File: score 9
Sequence: 1 contigrama 9
Scoring table: HMMTPT, HMC
Gap: 10.0 ; Gap: 1.0

Searched: 441382 seqs, 1331831 residues

Total number of hits satisfying chosen parameters: 68786

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2.6/podbase/1/nas/9A_COMB.seq.*
3: /cgn2.6/podbase/1/nas/9A_COMB.seq.*
4: /cgn2.6/podbase/1/nas/9A_COMB.seq.*
5: /cgn2.6/podbase/1/nas/PTGNS_COMB.seq.*
6: /cgn2.6/podbase/1/nas/mcdiff1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit.
and as derived by analysis of the pool score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
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7	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
8	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
9	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
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16	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
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23	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
24	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
25	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
26	66.7	9	1	US-08-411-020-1	Sequence 1, Appl
27	66.7	9	1	US-08-411-020-1	Sequence 1, Appl

c 28	66.7	9	1	US-08-410-7798-6	Sequence 5, Appl
c 29	66.7	9	1	US-08-410-7798-23	Sequence 23, Appl
c 30	66.7	9	1	US-08-410-7798-23	Sequence 23, Appl
c 31	66.7	9	1	US-08-410-7798-26	Sequence 26, Appl
c 32	66.7	9	1	US-08-410-7798-28	Sequence 28, Appl
c 33	66.7	9	1	US-08-410-7798-28	Sequence 28, Appl
c 34	66.7	9	1	US-08-410-7798-28	Sequence 28, Appl
c 35	66.7	9	1	US-08-410-7798-31	Sequence 31, Appl
c 36	66.7	9	1	US-08-410-7798-31	Sequence 31, Appl
c 37	66.7	9	1	US-08-410-7798-33	Sequence 33, Appl
c 38	66.7	9	1	US-08-410-7798-33	Sequence 33, Appl
c 39	66.7	9	1	US-08-410-7798-35	Sequence 35, Appl
c 40	66.7	9	1	US-08-410-7798-35	Sequence 35, Appl
c 41	66.7	9	1	US-08-410-7798-35	Sequence 35, Appl
c 42	66.7	9	2	US-08-853-091-25	Sequence 25, Appl
c 43	66.7	9	2	US-08-853-091-25	Sequence 25, Appl
c 44	66.7	9	2	US-08-853-091-26	Sequence 26, Appl
c 45	66.7	9	2	US-08-853-091-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-411-020-1
Patent No. 5712094
GENERAL INFORMATION: H. MART
APPLICANT: LAMU, I. PETER
APPLICANT: CHAM, SHU-SHIN TIAN
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
NUMBER OF SEQUENCES: 59
ADDRESSER: Ligand Pharmaceuticals Incorporated
STREET: 9933 Towne Centre Drive
CITY: San Diego
STATE: CA 92121
COUNTRY: US
CLASSIFICATION: 016-0030 US
CURRENT APPLICATION DATA: 08/411,020
APPLICATION NUMBER: 08/411,020
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0030 US
TELEPHONE: (619) 550-7875
TELEFAX: (619) 555-3906
INVENTOR CHARACTERISTICS:
LENGTH: 9 base pairs
STR: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: SYNTHETIC DNA
Query Match: 66.7%; Score 6; DB 1; Length 9;
Best local Similarity: 100.0%; Pred. No. 3.2e+07
Matches 9; Consecutive 0; Mismatches 0; Gaps 0;
1 TTCNNNGAA 9

1 INFORMATION FOR SEQ ID NO: 10:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 base pairs
 4 TYPE: nucleic acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: other nucleic acid
 8 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 9 DESCRIPTION: SYNTHETIC DNA
 10 US-08-411-020-10

Query Match 66.7% Score 6: DB 1: Length 9:
 Best Local Similarity 66.7%: Pctd No. 3.2e+07
 Mismatches 6: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

1 TTTCCGGA 9
 1111111
 Db 9 TTTCCGGA 1

1 RESULT 5
 2 US-08-411-020-11
 3 Sequence 11: Application US/08411020
 4 Patent No. 571064
 5 GENERAL INFORMATION:
 6 APPLICANT: SEIDEL, H. MARTI
 7 INVENTOR: CHAN, SHIN-SHAY TIAN
 8 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 9 DETECTING MODULATORS OF CYTOKINE ACTION
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Ligand Pharmaceuticals Incorporated
 12 9393 Towne Centre Drive
 13 CITY: San Diego
 14 STATE: California
 15 ZIP: 92121
 16 COMPUTER READABLE FORM: 41x
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: PATENTL RELEASE #1.0, version #1.30
 20 CURRENT APPLICATION DATA:
 21 FILING DATE: 27-Mar-1995
 22 CLASSIFICATION: 415
 23 NAME: Jurgensen, Thomas E.
 24 REGISTRATION NUMBER: 34,195
 25 TELEPHONE: (619) 550-7675
 26 INFORMATION: INFORMATION:
 27 TELEPHONE: (619) 550-7675
 28 INFORMATION FOR SEQ ID NO: 11:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 9 base pairs
 31 TYPE: nucleic acid
 32 STRANDEDNESS: single
 33 TOPOLOGY: linear
 34 MOLECULE TYPE: other nucleic acid
 35 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 36 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,"
 37 SYNTHETIC DNA"
 38 US-08-411-020-11

1 INFORMATION FOR SEQ ID NO: 10:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 base pairs
 4 TYPE: nucleic acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: other nucleic acid
 8 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 9 DESCRIPTION: SYNTHETIC DNA
 10 US-08-411-020-11

Query Match 66.7% Score 6: DB 1: Length 9:
 Best Local Similarity 66.7%: Pctd No. 3.2e+07
 Mismatches 6: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

1 TTTCCGGA 9
 1111111
 Db 9 TTTCCGGA 1

1 INFORMATION FOR SEQ ID NO: 10:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 base pairs
 4 TYPE: nucleic acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: other nucleic acid
 8 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 9 DESCRIPTION: SYNTHETIC DNA
 10 US-08-411-020-11

Query Match 66.7% Score 6: DB 1: Length 9:
 Best Local Similarity 66.7%: Pctd No. 3.2e+07
 Mismatches 6: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

1 TTTCCGGA 9
 1111111
 Db 9 TTTCCGGA 1

1 RESULT 6
 2 US-08-411-020-11/c
 3 Sequence 11: Application US/08411020
 4 Patent No. 571064
 5 GENERAL INFORMATION:
 6 APPLICANT: SEIDEL, H. MARTI
 7 INVENTOR: CHAN, SHIN-SHAY TIAN
 8 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 9 DETECTING MODULATORS OF CYTOKINE ACTION
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Ligand Pharmaceuticals Incorporated
 12 9393 Towne Centre Drive
 13 CITY: San Diego
 14 STATE: California
 15 ZIP: 92121
 16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: PC-DOS/MS-DOS
 20 SOFTWARE: PatentL Release #1.0, version #1.30
 21 CURRENT APPLICATION DATA:
 22 FILING DATE: 27-Mar-1995
 23 CLASSIFICATION: 415
 24 NAME: Jurgensen, Thomas E.
 25 REGISTRATION NUMBER: 34,195
 26 TELEPHONE: (619) 550-7675
 27 INFORMATION: INFORMATION:
 28 TELEPHONE: (619) 550-7675
 29 INFORMATION FOR SEQ ID NO: 11:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 9 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35 MOLECULE TYPE: other nucleic acid
 36 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 37 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,"
 38 SYNTHETIC DNA"
 39 US-08-411-020-11

1 INFORMATION FOR SEQ ID NO: 10:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 base pairs
 4 TYPE: nucleic acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: other nucleic acid
 8 FUNCTION: DETECTING MODULATORS OF CYTOKINE ACTION
 9 DESCRIPTION: SYNTHETIC DNA
 10 US-08-411-020-11

Query Match 66.7% Score 6: DB 1: Length 9:
 Best Local Similarity 66.7%: Pctd No. 3.2e+07
 Mismatches 6: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

1 TTTCCGGA 9
 1111111
 Db 9 TTTCCGGA 1

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release 1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08/04/90
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nathan Thomas E.
FOLDER NUMBER: 1156
REFERENCE NUMBER: 1156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-0275
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDS: single
TOPOLOGY: linear
MODULE TYPE: other nucleic acid
FUNCTION: other
DESCRIPTION: SYNTHETIC DNA

RESULT 8
 1. Sequence 12, Application US/08/11020
 2. Patent no. 3712694
 3. APPLICATION INFORMATION:
 4. APPLICANT: GIBSON, H. MARTI
 5. APPLICANT: LABB, I. PETER
 6. APPLICANT: CHAN, SHIN SHAW TAN
 7. TITLE OF INVENTION: ASSOCIATED FINANCIAL
 8. NUMBER OF SEQUENCES: 59
 9. ADDRESS: 15000
 10. STREET: 9931 Towne Circle Drive
 11. STATE: San Diego
 12. COUNTRY: US
 13. CIT: 9212
 14. COMPILED BY: ELEGY FROM
 15. MEDIUM TYPE: Floppy disk
 16. COMPILER: IBM PC compatible
 17. SOFTWARE: Microsoft Windows DOS
 18. CURRENT APPLICATION DATA: Version #1.30
 19. FILE NAME: US08/11020
 20. CLASSIFICATION: 435
 21. ANNOTATION/ABSTRACT INFORMATION:
 22. REGISTRATION NUMBER: 34,199
 23. REFERENCE/DOCKET NUMBER: 016-0030 US
 24. TELEPHONE: (619) 550-9578
 25. TELEFAX: (619) 555-3906
 26. E-MAIL: FOR SRO TO NO: 12;
 27. INSTRUCTIONS: 9 base pairs

07	1	TTCTTCAA	1	66.7%	Score 6:	DB 1:	Length 9:	0:	Gaps 0:
08	9	TTCTTCAA	1	66.7%	Prd: No. 3.2e-07	0:	Mismatches 5:	Indels 0:	Gaps 0:

RESULTS
US-08-411-020-13
Sequence 13, Application us/08411020

Patient No. 9712094
DOB: 06/11/1955
APPLICANT: SEITZ, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: SHEN-SHIN, TIAN
TITLE OF INVENTION: ANTIBODIES ASSOCIATED REAGENTS FOR
CYTOKINE DETECTION
CORRESPONDENCE ADDRESS:
ADDRESSER: Ligand Pharmaceuticals Incorporated
CITY: San Diego
STATE: California
ZIP: 92121
COMPUTER READABLE FORM:
CODING SYSTEM: POLY-DISK
CODING SYSTEM: IBM-PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT RELEASE #1.0, Version #1.30
COPYRIGHT YEAR: 1995
APPLICATION NUMBER: US/08411_020
CLINTG DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jurgenen, Thomas E.
REFERENCE/COCKET NUMBER: .016-.030 US
TELECOMMUNICATION INFORMATION:
TEL-FAX: (619) 513-3906
INFORMATION FOR SEQ ID NO: 13:
LENGTH: 9 base pairs;
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
RESCRIPTION: OTHER NUCLEIC ACID,
SYNTHETIC DNA

US-08-411-020-13

Query Match
Heat Link Similarity 66.7% Score 6; DB 1; Length %;
Matches 1; Conservative 0; Mismatches 3; Indels 0;
Oy 1 TTCNNCAAA G
DB 1 TTCCACAA 9

RESULT 10
US-08-411-020-13/c

RESULT 10
US-08-411-020-13/c

Sequence 13, Application US/08411020
 RESEARCH INFORMATION:
 APPLICANT: SEIDEL, H. MARZI
 APPLICANT: LAM, H. PERRY
 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 DETECTING MODULATORS OF CYTOKINE ACTION
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 3900 Stone Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08411100
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 435
 ATOMIZER/AGENT INFORMATION:
 NAME: Jurgensen, Thomas E.
 REGISTRATION NUMBER: 34,155
 TELEPHONE: (619) 550-7875
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SSO ID NO: 0030.US
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODIFICATION: none
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-411-020-13
 Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Pval No. 3.2e-07;
 Matches 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 TTCC000A 9
 9 TTCC00A 1

RESULT 11
 US-08-369-79-25
 Sequence 25, Application US/08369796
 RESEARCH INFORMATION:
 APPLICANT: James E. Darnell, Jr.
 APPLICANT: Zhang Zhong
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 TRANSDUCTION AND ACTIVATION OF TRANSCRIPTION (STAT) PROTEINS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 3900 Stone Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08369796
 CLASSIFICATION: 435
 ATOMIZER/AGENT INFORMATION:
 NAME: Jurgensen, Thomas E.
 REGISTRATION NUMBER: 34,155
 TELEPHONE: (619) 550-7875
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SSO ID NO: 0030.US
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 MODIFICATION: none
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-369-796-25
 Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Pval No. 3.2e-07;
 Matches 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 TTCC000A 9
 1 TTCC00A 9

RESULT 12
 US-08-369-796-25/C
 Sequence 25, Application US/08369796
 RESEARCH INFORMATION:
 APPLICANT: James E. Darnell, Jr.
 APPLICANT: Zhang Zhong
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 TRANSDUCTION AND ACTIVATION OF TRANSCRIPTION (STAT) PROTEINS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 3900 Stone Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08369796
 CLASSIFICATION: 435
 ATOMIZER/AGENT INFORMATION:
 NAME: Jurgensen, Thomas E.
 REGISTRATION NUMBER: 34,155
 TELEPHONE: (619) 550-7875
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SSO ID NO: 25;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 MODIFICATION: none
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-369-796-25
 Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Pval No. 3.2e-07;
 Matches 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 TTCC000A 9
 1 TTCC00A 9

LENGTH: 9 base pairs
 TYPE: nucleic acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA synthetic probe
 AMPLI-SENS: NO

US-08-369-796-25

Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Freq. No. 3.2e+07

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 TCCGCGA 9

DB 9 TTCGCGA 1

SEQUENCE 13

US-08-369-796-26

Sequence 26; Application US/0816976

Patent No. 5716222

GENERAL INFORMATION: F. Darnell, Jr.

APPLICANT: Eliong Wen

INVENTOR: Eliong Wen

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/369-796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

NAME: Jackson Bq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

COMPUTER READABLE FORM:

COMPUTER: IBM compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CHARACTER SET: ASCII

APPLICATION NUMBER: US/08/369-796

FILING DATE: 06-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bq., David A.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE: 9 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA synthetic probe

AMPLI-SENS: NO

US-08-369-796-26

Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Freq. No. 3.2e+07

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 TCCGCGA 9

RESULT 14

US-08-369-796-26/2

Sequence 26; Application US/0816976

Patent No. 5716222

GENERAL INFORMATION: F. Darnell, Jr.

APPLICANT: Eliong Wen

INVENTOR: Eliong Wen

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/369-796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

NAME: Jackson Bq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

COMPUTER READABLE FORM:

COMPUTER: IBM compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CHARACTER SET: ASCII

APPLICATION NUMBER: US/08/369-796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

NAME: Jackson Bq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE: 9 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA synthetic probe

AMPLI-SENS: NO

US-08-369-796-26

Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Freq. No. 3.2e+07

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 TCCGCGA 9

DB 9 TTCGCGA 1

SEQUENCE 15

US-08-369-796-27

Sequence 27; Application US/0816976

Patent No. 5716222

GENERAL INFORMATION: F. Darnell, Jr.

APPLICANT: Eliong Wen

INVENTOR: Eliong Wen

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/369-796

FILING DATE: 06-JAN-1995

RESULT 15

US-08-369-796-27

Sequence 27; Application US/0816976

Patent No. 5716222

GENERAL INFORMATION: F. Darnell, Jr.

APPLICANT: Eliong Wen

INVENTOR: Eliong Wen

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/369-796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

NAME: Jackson Bq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

COMPUTER READABLE FORM:

COMPUTER: IBM compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CHARACTER SET: ASCII

APPLICATION NUMBER: US/08/369-796

FILING DATE: 06-JAN-1995

CLASSIFICATION: 435

NAME: Jackson Bq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

FAX: 201 487-5800

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07603A

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE: 9 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA synthetic probe

AMPLI-SENS: NO

US-08-369-796-26

Query Match 66.7% Score 6; DB 1; Length 9;
 Best Local Similarity 66.7%; Freq. No. 3.2e+07

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 TCCGCGA 9

DB 9 TTCGCGA 1

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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
VERSION: Microsoft Windows 4.10, Version 41.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/169,796
CLASSIFICATION: 435-1995
ATTORNEY/AGENT INFORMATION:
  NAME: [REDACTED]
  REGISTRATION NUMBER: 446744
  REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 201 343-7200
  TELEFAX: 201 343-1684
  INTERNET: [REDACTED]
  IP NO: 27
SEQUENCE CHARACTERISTICS:
  LENGTH: 9 base pairs
  TYPE: double-stranded
  STRANDEDNESS: double
  TOPOLOGY: linear
MOLECULE TYPE: DNA synthetic probe
  ORGANISM: [REDACTED]
  AVI-SHINE: NO
US-08-369-796-27

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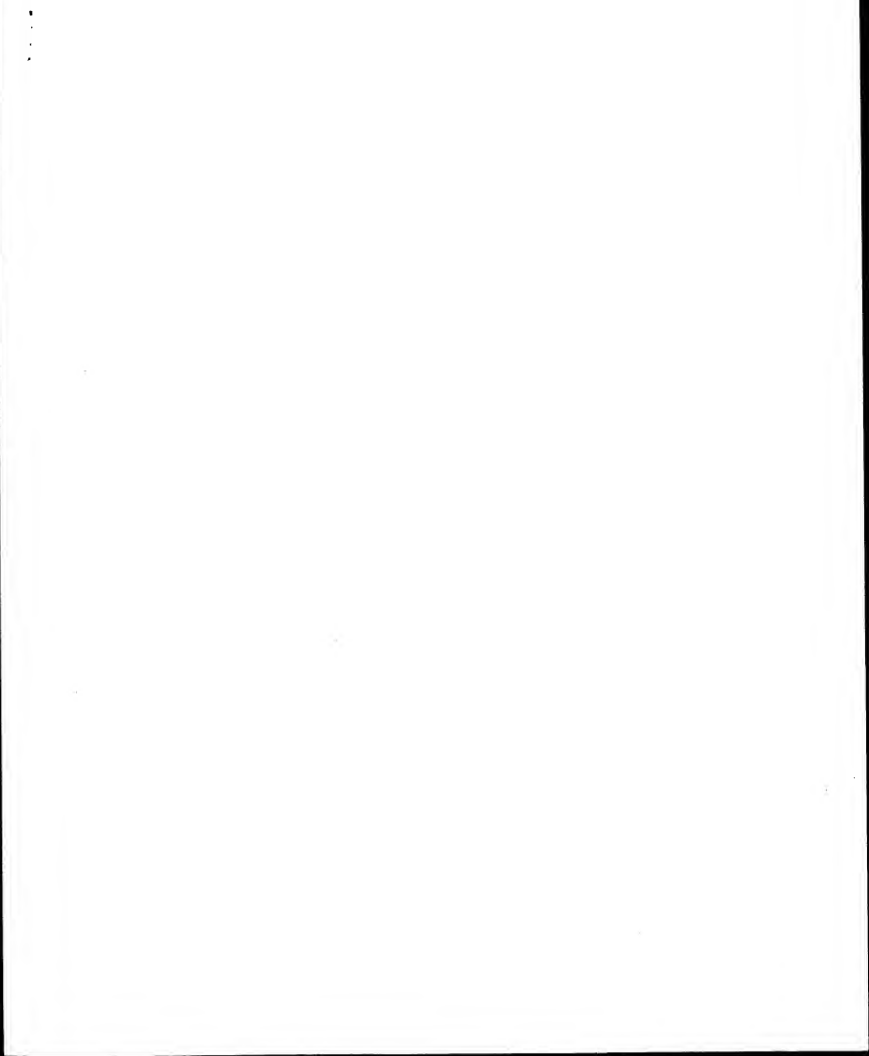
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 Best Local Similarity 66.7%; Pred.No. 3.2e+07;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 TTCCGCGAA 9
DB 1 TTCCGCGAA 9

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Search completed: December 25, 2002, 20:21:58
 Job time: 53 secs



claim 13, 17, 20
sequences

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AGAATTCAGAGATATCA 18
 Db 1 AGAATTCAGAGATATCA 18
 RESULT 2
 US-09-522-217-59
 Sequence 56: Application US/0952217
 Patent No. 6307024
 GENERAL INFORMATION:
 APPLICANT: No. 6307024K, Julia E.
 APPLICANT: Inventor: Scott R.
 APPLICANT: Foster, Cindy A.
 APPLICANT: Speercher, Cindy A.
 APPLICANT: Gross, Jane A. D.
 APPLICANT: Johnson, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE RAMPHALI LIGAND
 CURRENT APPLICATION NUMBER: US/09/522 217
 CURRENT FILING DATE: 2000-03-09
 PUBLICATION DATE: 1999-02-09
 EXAMINER FILING DATE: 1999-02-09
 EXAMINER APPLICATION NUMBER: US 60/423 904
 EXAMINER FILING DATE: 1999-02-09
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FASTSD for Windows version 3.0
 SEQ ID NO 59
 LENGTH: 100
 ORGANISM: Artificial Sequence
 FEATURE:
 ORGANIZATION: Oligonucleotide EC12749
 US-09-522-217-59
 Query Match 56.7% Score 18, DB 4; Length 100;
 Similarity 100.0%; Pred. No. 8.6;
 Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AGAATTCAGAGATATCA 18
 Db 67 AGAATTCAGAGATATCA 84
 RESULT 3
 US-09-522-217-60
 Sequence 60: Application US/0952217
 Patent No. 6307024
 GENERAL INFORMATION:
 APPLICANT: No. 6307024K, Julia E.
 APPLICANT: Inventor: Scott R.
 APPLICANT: Speercher, Cindy A.
 APPLICANT: Foster, Cindy A.
 APPLICANT: Gross, Jane A. D.
 APPLICANT: Johnson, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE RAMPHALI LIGAND
 CURRENT APPLICATION NUMBER: US/09/522 217
 CURRENT FILING DATE: 2000-03-09
 PUBLICATION DATE: 1999-02-09
 EXAMINER FILING DATE: 1999-02-09
 EXAMINER APPLICATION NUMBER: US/09/522 217
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FASTSD for Windows version 3.0
 SEQ ID NO 60
 LENGTH: 100
 ORGANISM: Artificial Sequence
 FEATURE:
 ORGANIZATION: Oligonucleotide EC12748
 US-09-522-217-60
 Query Match 85.7% Score 18, DB 4; Length 100;
 Similarity 100.0%; Pred. No. 8.6;
 Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AGAATTCAGAGATATCA 18
 Db 38 AGAATTCAGAGATATCA 21

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AGAATTCAGAGATATCA 18
 Db 38 AGAATTCAGAGATATCA 21
 RESULT 4
 US-09-140-804-46
 Sequence 46: Application US/0910804
 Patent No. 6319700
 GENERAL INFORMATION:
 APPLICANT: Inventor: Jacqueline M.
 APPLICANT: Sheppard, Paul O.
 TITLE OF INVENTION: PEPTIDE-SPECIFIC PROTEIN HOMOLOGS
 FILE REFERENCE: 97-49
 CURRENT APPLICATION NUMBER: US/09/140,804
 CURRENT FILING DATE: 1997-08-26
 EXAMINER FILING DATE: 1997-08-26
 EXAMINER APPLICATION NUMBER: 60/056,983
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: FASTSD for Windows version 3.0
 SEQ ID NO 46
 LENGTH: 58
 ORGANISM: Artificial Sequence
 FEATURE:
 ORGANIZATION: Oligonucleotide EC14819
 US-09-140-804-46
 Query Match 65.5% Score 14.5, DB 4; Length 58;
 Similarity 81.0%; Pred. No. 2.8e02;
 Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 AGAATTCAGAGATATCA 21
 Db 14 AGAATTCAGAGATATCA 34
 RESULT 5
 US-09-17-043-22
 Sequence 43: Application US/0911043
 Patent No. 6207442
 GENERAL INFORMATION:
 APPLICANT: Inventor: Christopher K.
 TITLE OF INVENTION: PLASID CONSTRUCTION BY HOMOLOGOUS
 RECOMBINATION
 TITLE OF INVENTION: RECOMBINATION
 CURRENT APPLICATION NUMBER: US/09/173,043
 CURRENT FILING DATE: 1998-10-15
 EXAMINER FILING DATE: 1998-10-15
 EXAMINER APPLICATION NUMBER: US/09/173,043
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FASTSD for Windows version 3.0
 SEQ ID NO 34
 LENGTH: 58
 ORGANISM: Artificial Sequence
 FEATURE:
 ORGANIZATION: Oligonucleotide EC14819

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/453.0903
 CLUSTER IDENTIFICATION: 05-304-1945
 CLUSTER DATE: 05-304-1945
 ATTORNEY/AGENT INFORMATION:
 NAME: VINCENT, MATTHEW P.
 REFERENCE/DOCKET NUMBER: MT002.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 812-7000
 TELEFAX: (617) 812-7000
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE INFORMATION:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: oligonucleotide
 US-08-453-090-24
 Query Match: 65.7%; Score 13.8; DB 1; Length 30;
 Best Local Similarity: 88.2%; Pred. No. 6,36e+02;
 Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;
 Oy: 3 ATTCTGAGGATCAAA 19
 Db: 20 ATTCGAGGATCAAAA 4

FIGURE 10
 US-08-332-420-54/C
 Sequence 54, Application US/08332420
 Patent No. 5744300N
 OTHER INFORMATION:
 APPLICANT: Masten H.K. Linsberg, et al.
 TITLE OF INVENTION: METHODS AND REAGENTS FOR THE
 DETECTION OF SEQUENCE-SPECIFIC DNA BINDING
 TITLE OF INVENTION: OF SEQUENCE-RELATED GENE
 NUMBER OF SEQUENCES: 70
 CLASSIFICATION: 435
 ADDRESS: 10000
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90011
 COMPUTER: IBM compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332.420
 CLUSTER IDENTIFICATION: 435
 CLUSTER DATE: 05-31-1994
 APPLICATION DATA: 08/235.100
 FILING DATE: April 29, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MATTHEW, RICHARD J.
 REFERENCE/DOCKET NUMBER: 210/941
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 955-0440
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE INFORMATION:
 LENGTH: 34
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-332-420-54
 Query Match: 64.8%; Score 13.5; DB 1; Length 34;
 Best Local Similarity: 88.0%; Pred. No. 7,48e+02;
 Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;
 Oy: 1 AGATTGAGGATCAAA 20
 Db: 32 AGATGAGGATCAAAAT 13

FIGURE 11
 US-07-941-363-1
 Sequence 11, Application US/07941363
 Patent No. 516886
 OTHER INFORMATION:
 APPLICANT: Lee, Stephen C.
 REFERENCE/DOCKET NUMBER: 100/1000
 APPLICANT: Linsch, Mark S.
 APPLICANT: Olus, Peter O.
 TITLE OF INVENTION: Method of Producing Recombinant
 NUMBER OF SEQUENCES: 9
 CLASSIFICATION: 435
 ADDRESS: 800 N. Lindbergh Blvd.
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63167
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/941.363
 CLUSTER IDENTIFICATION: 05-304-1945
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 34,547
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 554-5400
 TELEFAX: (314) 554-9009
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE INFORMATION:
 LENGTH: 37 base pairs
 TYPE: NUCLEIC ACID
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-07-941-363-1
 Query Match: 64.8%; Score 13.5; DB 1; Length 37;
 Best Local Similarity: 80.0%; Pred. No. 7,48e+02;
 Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;
 Oy: 1 AGATTGAGGATCAAA 20
 Db: 1 AGATGAGGATCAAAAT 20

FIGURE 12
 US-09-143-634-28/C
 Sequence 28, Application US/0914364
 Patent No. 6,36e+02;
 OTHER INFORMATION:
 APPLICANT: Zdanovsky, Aleey G.
 TITLE OF INVENTION: EXPRESSION OF CYTOSOLIC TOXINS AND PROTEINS

ATTORNEY/AGENT INFORMATION:
1 NAME: Saidman, Stephanie L.
2 REGISTRATION NUMBER: 33779
3 REGISTRATION EXPIRATION DATE: 12/31/2003
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (619)552-1311
6 FAX: (619)552-1311
7 INFORMATION FOR SPD ID NO: 4:
8 SEQUENCE CHARACTERISTICS:
9 NAME: 4B base pairs
10 TYPE: unique
11 STRANDEDNESS: single
12 TOPOLOGY: unknown
13 METHOD: Sanger
14 PCR-DB91-06452-4: DNA (genomic)
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GenCode version 5.1.3
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OK nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:49 : Search time 352 Seconds

71359 Million cell updates/sec

Title: SCHMIDT075

Sequence: 1 tctctgga 9

Scoring table: Dayp 10.0, Expect 1.0

Searched: 2185239 seqs, 11299319 residues

Total number of hits satisfying chosen parameters: 2300332

Minimum hit seq length: 0

Maximum hit seq length: 100

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 403 summaries

Database:

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24: /SID52/sgcatv/geneseq/geneeqn-emb/NA2003.DMT.*

SUMMARIES

Prod. No. 14 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Query	length	na	ID	Description
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2	66.7	9	16	AA114121	Cytokine responsive
3	66.7	9	16	AA114122	Cytokine responsive
4	66.7	9	16	AA114123	Cytokine responsive
5	66.7	9	16	AA114124	Cytokine responsive
6	66.7	9	16	AA114125	Cytokine responsive
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8	66.7	9	16	AA114127	Cytokine responsive
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C 15	66.7	9	16	AA114145	Cytokine responsive
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C 21	66.7	9	16	AA114151	Cytokine responsive
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C 94	66.7	9	16	AA114224	Cytokine responsive
C 95	66.7	9	16	AA114225	Cytokine responsive
C 96	66.7	9	16	AA114226	Cytokine responsive

detecting the presence of transcriptional regulatory protein in a sample

Diagnosis: Page 18; 135pp; English.

The present oligonucleotide comprises a regulatory element activated transcriptional regulatory protein in response to a signal, wherein the signal is a cytokine. The regulatory element is a spacer regulatory element can be used to detect the presence of a transcriptional regulatory protein in a sample, and in assays for the diagnosis of gene transcription. The identified cpgs may be used to detect the presence of a transcriptional regulatory element in a sample, and in assays for the diagnosis of gene transcription. The identified cpgs may be used to treat cytokine-induced disease states, or to ameliorate disease states caused by cytokine deficiency, e.g. inflammation, anemia, cytopenia and (pre)neoplastic conditions.

Sequence 9 BP; 2 A; 1 C; 1 G; 2 T; 3 other;

Query Match: 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.4e+08;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTTCCNNAGA 9
1 TTTCCNNAGA 9

AP114155 standard; DNA; 9 BP.
AP114155 (first entry)

30-MAY-1996 (first entry)

Cytokine responsive DNA spacer regulatory element.

Regulatory element; transcriptional regulatory protein; signaling molecule; DNA spacer; agonist; antagonist; anemia; gene transcription; inflammation; cytopenia; cancer; ss.

Synthetic.

W0932482-32.

26-OCT-1995.

10-APR-1995; 95NO-US04177.

27-MAR-1995; 95NO-0410780.

14-MAR-1994; 94OS-028935.

(LICOR) LICOR PHARM INC.

Lamb TP, Seidel HM.

WPI; 1995-73737/48.

DNA spacer regulatory elements responsive to cytokine(s) - for detecting the presence of transcriptional regulatory protein in a sample

Disclosures: Page 18; 135pp; English.

The present oligonucleotide comprises a regulatory element activated transcriptional regulatory protein in response to a signal, wherein the signal is a cytokine. The regulatory element is a spacer regulatory element can be used to detect the presence of a transcriptional regulatory protein in a sample, and in assays for the diagnosis of gene transcription. The identified cpgs may be used to treat cytokine-induced disease states, or to ameliorate disease states caused by cytokine deficiency, e.g. inflammation, anemia, cytopenia and (pre)neoplastic conditions.

Inflammation, anemia, cytopenia and (pre)neoplastic conditions.

Sequence 9 BP; 2 A; 1 C; 1 G; 2 T; 3 other;

Query Match: 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.4e+08;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTTCCNNAGA 9
1 TTTCCNNAGA 1

AP114155 standard; DNA; 9 BP.
AP114155 (first entry)

30-MAY-1996 (first entry)

Cytokine responsive DNA spacer regulatory element.

Regulatory element; transcriptional regulatory protein; signaling molecule; DNA spacer; agonist; antagonist; anemia; gene transcription; inflammation; cytopenia; cancer; ss.

Synthetic.

W0932482-32.

26-OCT-1995.

10-APR-1995; 95NO-US04177.

27-MAR-1995; 95NO-0410780.

14-MAR-1994; 94OS-028935.

(LICOR) LICOR PHARM INC.

Lamb TP, Seidel HM.

WPI; 1995-73737/48.

DNA spacer regulatory elements responsive to cytokine(s) - for detecting the presence of transcriptional regulatory protein in a sample

Disclosures: Page 18; 135pp; English.

The present oligonucleotide comprises a regulatory element activated transcriptional regulatory protein in response to a signal, wherein the signal is a cytokine. The regulatory element is a spacer regulatory element can be used to detect the presence of a transcriptional regulatory protein in a sample, and in assays for the diagnosis of gene transcription. The identified cpgs may be used to treat cytokine-induced disease states, or to ameliorate disease states caused by cytokine deficiency, e.g. inflammation, anemia, cytopenia and (pre)neoplastic conditions.

Sequence 9 BP; 2 A; 1 C; 1 G; 2 T; 3 other;

Query Match: 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.4e+08;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 TTTCCNNAGA 9
1 TTTCCNNAGA 9

RESULT 4

DR WPI: 1995-73797/48.
 CC DNA spacer regulatory elements responsive to cytokine(s) - for
 PT detecting the presence of transcriptional regulatory protein in a
 sample
 XX
 PS Claim 7, Page 125, 135pp: English.
 CC The present oligonucleotide comprises a regulatory element
 CC activated transcriptional regulatory protein in response to a
 CC signaling mol., i.e. a cytokine. This cytokine responsive DNA
 CC spacer regulatory element can be used to detect the presence of
 CC a transcriptional regulatory protein in a sample, and in assays
 CC for (anti)agonists of gene transcription. The identified cpds.
 CC for (anti)agonists of gene transcription, the identified cpds.
 CC ameliorate disease states caused by cytokine deficiency, e.g.
 CC inflammation, anemia, cytopenia and (pre)neoplastic conditions.
 XX
 CC Sequence 9 BP: 3 A; 2 C; 1 G; 3 T; 0 other.
 DE Query Match 66.7% Score 6; DB 16; Length 9;
 XX Best Local Similarity 66.7%; Pctd No. 2.4e+08;
 XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 GY 1 TTCNNNAA 9
 DB 9 TTCGCGAA 1

RESULT 7
 ID AAT14145 standard-DNA; 9 BP.
 AC AAT14145;
 XX 29-MAR-1996 (first entry)
 DE Cytokine responsive DNA spacer regulatory element.
 XX
 DE Regulatory element: transcriptional regulatory protein;
 XX signaling molecule; DNA spacer; agonist; antagonist; anemia;
 XX gene transcription; inflammation; cytopenia; cancer; ss.
 XX Synthetic.
 XX W09528482-A2.
 XX 10-APR-1995; 95NO-US64477.
 XX 26-OCT-1995.
 XX 27-MAR-1995; 95US-0410780.
 XX 14-MAR-1994; 94US-0228935.
 XX (LICOR-) LICORND PHARM INC.
 XX
 XX "Lamb IP, Seidel IM;
 WPI: 1995-73797/48.
 CC DNA spacer regulatory elements responsive to cytokine(s) - for
 PT detecting the presence of transcriptional regulatory protein in a
 sample
 XX
 PS Claim 7, Page 125, 135pp: English.
 CC The present oligonucleotide comprises a regulatory element
 CC activated transcriptional regulatory protein in response to a
 CC signaling mol., where x is 4-7, and the regulatory element binds to a
 CC transcriptional regulatory protein in a sample, and in assays
 CC for (anti)agonists of gene transcription. The identified cpds.
 CC ameliorate disease states caused by cytokine deficiency, e.g.
 CC inflammation, anemia, cytopenia and (pre)neoplastic conditions.
 XX
 CC Sequence 9 BP: 3 A; 3 C; 1 G; 2 T; 0 other.

CC for (anti)agonists of gene transcription. The identified cpds.
 CC may be used to treat cytokine-induced disease states, or to
 CC detect the presence of transcriptional regulatory protein in a
 CC inflammation, anemia, cytopenia and (pre)neoplastic conditions.
 XX
 XX Sequence 9 BP: 3 A; 3 C; 1 G; 2 T; 0 other.
 DE Query Match 66.7% Score 6; DB 16; Length 9;
 XX Best Local Similarity 66.7%; Pctd No. 2.4e+08;
 XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 GY 1 TTCNNNAA 9
 DB 1 TTCGCGAA 9

RESULT 8
 ID AAT14145/c
 AC AAT14145;
 XX 29-MAR-1996 (first entry)
 DE Cytokine responsive DNA spacer regulatory element.
 XX
 DE Regulatory element: transcriptional regulatory protein;
 XX signaling molecule; DNA spacer; agonist; antagonist; anemia;
 XX gene transcription; inflammation; cytopenia; cancer; ss.
 XX Synthetic.
 XX W09528482-A2.
 XX 10-APR-1995; 95NO-US64477.
 XX 27-MAR-1995; 95US-0410780.
 XX 14-MAR-1994; 94US-0228935.
 XX (LICOR-) LICORND PHARM INC.
 XX
 XX "Lamb IP, Seidel IM;
 WPI: 1995-73797/48.
 CC DNA spacer regulatory elements responsive to cytokine(s) - for
 PT detecting the presence of transcriptional regulatory protein in a
 sample
 XX
 PS Claim 7, Page 125, 135pp: English.
 CC The present oligonucleotide comprises a regulatory element
 CC activated transcriptional regulatory protein in response to a
 CC signaling mol., where x is 4-7, and the regulatory element binds to a
 CC transcriptional regulatory protein in a sample, and in assays
 CC for (anti)agonists of gene transcription. The identified cpds.
 CC ameliorate disease states caused by cytokine deficiency, e.g.
 CC inflammation, anemia, cytopenia and (pre)neoplastic conditions.
 XX
 CC Sequence 9 BP: 3 A; 3 C; 1 G; 2 T; 0 other.

Query Match 66.7% Score 6; DB 16; Length 9;
 Best Local Similarity 66.7%; Pctd No. 2.4e+08;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 GY 1 TTCNNNAA 9
 DB 9 TTCGCGAA 1

RESULT 9
XX ANTI1417/0
XX ID ANTI1417 standard; DNA: 9 BP.
XX ANTI1417:
XX ANTI1417:
XX 28-MAR-1995: (first entry)
XX Cytokine responsive DNA spacer regulatory element.
XX Regulatory element; transcriptional regulatory protein;
XX signaling molecule; DNA spacer; agonist; antagonist; anemata;
XX gene transcription; inflammation; cytopanels; cancer; ss.
XX Synthetic.
XX MO528482-A2.
XX 26-OCT-1995.
XX 10-APR-1995: 95NO-0504477.
XX 27-MAR-1995: 95US-0410780.
XX 14-APR-1994: 94US-0228935.
XX (LIGON-) LIGAND PHARM INC.
XX Lamb IP, Setdel IM;
XX NEI: 1995-373797/48.
XX DNA spacer regulatory elements responsive to cytokines) - for
XX detecting the presence of transcriptional regulatory protein in a
XX sample
XX
XX Claim 7; Page 125; 135pp; English
XX
XX The present oligonucleotide comprises a regulatory element
XX activated transcriptional regulatory element binds an
XX signaling mol., i.e. a cytokine. This cytokine responsive DNA
XX spacer regulatory element can be used to detect the presence of
XX for (ant)agonists of gene transcription. The identified spds
XX may be used to treat cytokine-induced disease states, or to
XX inflammation, anemata, cytopanels and (pre)cancerous conditions.
XX
XX Sequence 9 BP; 2 A; 1 G; 5 T; 0 other:
XX
XX Query Match 66.7%; Score 6; DB 16; Length 9;
XX Best Local Similarity 66.7%; Pred. No. 2,4e+08;
XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 TTTCCNNCA 9
XX 1 TTTTCTTCA 9
XX 1 TTTCTTCA 9
XX
XX RESULT 10
XX ANTI1417/0
XX ID ANTI1417 standard; DNA: 9 BP.
XX ANTI1417:
XX ANTI1417:
XX 29-MAR-1995: (first entry)
XX Cytokine responsive DNA spacer regulatory element.
XX Regulatory element; transcriptional regulatory protein;
XX signaling molecule; DNA spacer; agonist; antagonist; anemata;
XX gene transcription; inflammation; cytopanels; cancer; ss.

XX gene transcription; inflammation; cytopanels; cancer; ss.
XX Synthetic.
XX MO528482-A2.
XX 26-OCT-1995.
XX 10-APR-1995: 95NO-0504477.
XX 27-MAR-1995: 95US-0410780.
XX 14-APR-1994: 94US-0228935.
XX (LIGON-) LIGAND PHARM INC.
XX Lamb IP, Setdel IM;
XX NEI: 1995-373797/48.
XX DNA spacer regulatory elements responsive to cytokines) - for
XX detecting the presence of transcriptional regulatory protein in a
XX sample
XX
XX Claim 7; Page 125; 135pp; English.
XX
XX The present oligonucleotide comprises a regulatory element
XX 77(N)A, where x is 4-7, and the regulatory element binds an
XX activated transcriptional regulatory protein in response to DNA
XX signaling molecule. This cytokine responsive DNA spacer regula-
XX tory element can be used to detect the presence of
XX a transcriptional regulatory protein in a sample, and in assays
XX for (ant)agonists of gene transcription. The identified spds
XX may be used to treat cytokine-induced disease states, or to
XX inflammation, anemata, cytopanels and (pre)cancerous conditions.
XX
XX Sequence 9 BP; 2 A; 1 G; 5 T; 0 other:
XX
XX Query Match 66.7%; Score 6; DB 16; Length 9;
XX Best Local Similarity 66.7%; Pred. No. 2,4e+08;
XX Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 TTTCCNNCA 9
XX 1 TTTTCTTCA 9
XX 1 TTTCTTCA 9
XX
XX RESULT 11
XX ANTI1410/0
XX ID ANTI1410 standard; DNA: 9 BP.
XX ANTI1410:
XX ANTI1410:
XX 29-MAR-1995: (first entry)
XX Cytokine responsive DNA spacer regulatory element.
XX Regulatory element; transcriptional regulatory protein;
XX signaling molecule; DNA spacer; agonist; antagonist; anemata;
XX gene transcription; inflammation; cytopanels; cancer; ss.
XX Synthetic.
XX MO528482-A2.
XX 26-OCT-1995.
XX 10-APR-1995: 95NO-0504477.
XX 27-MAR-1995: 95US-0410780.
XX 14-APR-1994: 94US-0228935.
XX (LIGON-) LIGAND PHARM INC.

```

XX XX Lamb II; scd6l [NM];
DR MM NM1_1995-73797/48.
PT detecting the presence of transcriptional regulatory protein in a
PS sample
PS PS Page 125; 139pp; English.
XX XX The present oligonucleotide comprises a regulatory element
XX CC TTTAGAA, where x is A, C, G or T, and said element binds an
XX CC activating transcriptional regulatory protein in response to a
XX CC activated transcriptional regulatory protein in response to a
XX XX Sequence 9 BP: 2 A; 3 C; 2 T; 0 other:
XX XX Query Match 66/74; Score 6; DB 16; Length 9;
XX XX Similarity 66/74; Pctid 66/74;
XX XX Method(s) 0; Conservative 0; Miscellaneous 0; Indels 0; Gaps 0;
DB 1 TTCCGCGA 9
XX XX RESULT 12
XX XX AMT4140 standard; DMM; 9 BP.
XX XX AMT4140
XX XX 5P-MW-1986 (first entry)
XX XX
XX XX Cytokine responsive DNA spacer regulatory element.
XX XX Regulatory element; Transcriptional regulatory protein;
XX MM signalling molecule; DNA spacer; agonist; antagonist; anemias;
XX MM gene transcription; inflammation; cytopenia; cancer; ss.
XX XX Synthetic.
XX XX K0528483-A2.
XX XX
XX XX 10-BPR-1995; 93M-USG0477.
XX XX
XX XX 7Y-MN-1995; 93SC-O410780.
XX XX 1I-BPR-1994; 94US-OZ2893.
XX PA (LIGAND LIGAND PHARM INC.)
XX PT Lamb II; scd6l [NM].
XX PT NM1_1995-73797/48.
XX PT
XX PT Claim 7; Page 125; 139pp; English.
XX XX The present oligonucleotide comprises a regulatory element
XX CC TTTAGAA, where x is A, C, G, and the regulatory element binds an
XX CC activated transcriptional regulatory protein in response to a

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[illegible]

OY 1 TTCNNMNA 9
 ||| |||
 DB 1 TTCGCCAGA 9

RESULT 14
 AMT14137 standard: DNA: 9 BP.

OY 29-MAY-1996 (first entry)

XX Cytokine responsive DNA spacer regulatory element.

XX Regulatory element; transcription; regulatory protein;
 XX signalling molecule; DNA spacer; agonist; antagonist; anemias;
 XX gene transcription; inflammation; cytopenia; cancer; ss.

XX Synthetic.

XX MO5928482-A2.

XX 26-OCT-1995.

XX 10-APR-1995: 95NM-050447.

XX 27-MAR-1995: 95IS-041078.

XX 14-APR-1994: 94OS-0228935.

XX (LIG4-) LIGAND PHARM INC.

XX Lamb IP, Solid1 IM;

XX WPI: 1995-37377/48.

XX DNA spacer regulatory elements responsive to cytokine(s) - for
 XX detecting the presence of transcriptional regulatory protein in a
 XX sample

XX Claim 7: Page 125: 135pp: English.

XX The present oligonucleotide comprises a regulatory element
 CC activated transcriptional, and the regulatory element binds an
 CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
 CC spacer regulatory element can be used to detect the presence of
 CC a transcriptional regulatory protein in a sample, and in assays
 CC for antagonists of gene transcription. The identified ends
 CC may be used to treat cytokine-induced disease states, or to
 CC inflammation, anemia, cytopenia and (pre)cancerous conditions.

XX Sequence 9 BP: 2 A; 2 C; 2 G; 3 T; 0 other;

XX Query Match: 66.7%; Score 6; DB 16; Length 9;

XX Matches: 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTCNNMNA 9
 ||| |||

DB 9 TTCGCCAGA 1

RESULT 15

AMT14137 standard: DNA: 9 BP.

XX AMT14137;

XX 29-MAY-1996 (first entry)

XX Cytokine responsive DNA spacer regulatory element.

XX Regulatory element; transcription; regulatory protein;
 XX signalling molecule; DNA spacer; agonist; antagonist; anemias;
 XX gene transcription; inflammation; cytopenia; cancer; ss.

XX Synthetic.

XX MO5928482-A2.

XX 26-OCT-1995.

XX 10-APR-1995: 95NM-050447.

XX 27-MAR-1995: 95IS-041078.

XX 14-APR-1994: 94OS-0228935.

XX (LIG4-) LIGAND PHARM INC.

XX Lamb IP, Solid1 IM;

XX WPI: 1995-37377/48.

XX DNA spacer regulatory elements responsive to cytokine(s) - for
 XX detecting the presence of transcriptional regulatory protein in a
 XX sample

XX Claim 7: Page 124: 135pp: English.

XX The present oligonucleotide comprises a regulatory element
 CC activated transcriptional regulatory protein in response to a
 CC signalling molecule, where x is 4-7, and the regulatory element binds an
 CC DNA spacer regulatory element can be used to detect the presence of
 CC a transcriptional regulatory protein in a sample, and in assays
 CC for antagonists of gene transcription. The identified ends
 CC may be used to treat cytokine-induced disease states, or to
 CC inflammation, anemia, cytopenia and (pre)cancerous conditions.

XX Sequence 9 BP: 2 A; 4 C; 1 G; 2 T; 0 other;

XX Query Match: 66.7%; Score 6; DB 16; Length 9;

XX Matches: 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTCNNMNA 9
 ||| |||

DB 1 TTCGCCAGA 9

Search completed: December 25, 2002, 18:15:50
 500 time : 265 secs

1 Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) and ligated to a pTZ19 vector. The Eco RI
and Eco RI sites of the modified pTZ19 vector library
were then digested with Eco RI and ligated to the
cDNA library. The cDNA library was then ligated to the
vector and was transformed into *E. coli* cells.
29 a 10 c 27 c 7 g 27 c

Query Match 65.5% Score 14.6; m 9; length 73;
Best Local Similarity 81.0%; Pred. No. 2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OR 1 AACTTTCAGATCAATCAAC 21
17 AACTTTCAGATCAATCAAT 37

LOCUS AM959026 63 bp mRNA linear EST 21-DEC-2000
DEFINITION MED1009 developing stem Medicago truncatula cDNA clone
ACCESSION AM959026
VERSION AM959026.2 GI:11957373
KEYWORDS
SOURCE barrel medic
ORGANISM Medicago truncatula
TAXID 3845
NCBI Taxonomy: Medicago truncatula
Medicago truncatula: Strophomena; Anthropophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Rosales;
Rosidae; eucrodis 1; Fabales; Fabaceae; Papilionoideae; Trifoliales;
1 (bases 1 to 63)
He X.-Z., Shadle, G., Scott, A. D., Harris, A. R., Gonzalez, R. A., Ball
R. A., Flores, R. R., Iman, J. T., Weller, J. M., May, G. D. and Dixon
J. P. 2001. The Samuel Roberts Noble Foundation
Medicago truncatula stem library
On Apr 14, 2000 this sequence version replaced GI:7549788.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Dixon JM
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7302
Email: fadkx@noble.org
Insert length: 685 Std Error: 0.00
Seq primer: TCCACAGCAAGATCAATCAAC
Location/Qualifiers
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/method="cDNA library"
Internal stem segments: Contains a mixture of
intermolecular stem segments and
16 c 5 g 11 t

BASE COUNT 31 a 16 c 5 g 11 t
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Best Local Similarity 91.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OR 5 TTTCAGATCAATCAAC 30
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RESULT 5
AA37380

LOCUS AA37380 97 bp DNA linear GSS 07-OCT-2000
DEFINITION Med25589 Mouse 10kb plasmid UTRC1M library Mus musculus genomic
ACCESSION AA37380
VERSION AA37380.1 GI:10651393
KEYWORDS
SOURCE house mouse
ORGANISM Mus musculus
TAXID 10090
NCBI Taxonomy: Mus musculus
Mus musculus: Chordata; Eumetazoa; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 97)
Dima, D., Aoyagi, A., Balke, M., Basciani, F., Dimal, B., Dimal, C.,
K. M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., 2001. Mouse scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2001)
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT
University of Utah
801 University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
Tel: 801 585 5177
Fax: 801 585 7177
Insert length: 10000 Std Error: 0.00
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High quality sequence accp: 97.
Location/Qualifiers
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/db_xref="taxon:10090"
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/note="Vector: FPC920608; Purified genomic DNA from M.
labialis C57BL/6J (Jax) was obtained from the Jackson
Laboratory (Bar Harbor, ME). The DNA was
hydrolyzed/shattered by repeated passages through a
needle. The DNA was then ligated to the adaptors and
was blunt end repaired with T4 DNA polymerase and
polymerase kinase. Adaptor oligonucleotides were
added to the blunt ends in high molar excess. The
adaptors were then ligated to the blunt ends. The
10.5 kb range using preparative agarose gel. For a 9.5 to
electrophoresis, vector DNA was prepared from a derivative
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
adapted vector DNA, and transformed into *E. coli* cells
chemically competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT 33 a 16 c 5 g 12 t
ORIGIN
Query Match 66.6% Score 14.4; m 9; length 97;
Best Local Similarity 91.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OR 4 TTTCAGATCAATCAAC 19
21 TTTCAGATCAATCAAC 36

RESULT 6
BM81599

Fri Dec 27 17:38:55 2002

us-09-744-875-1.rst

Page 8

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OY      2  GATTCTAGGATTCAA 18
          || || | || || || ||
Db      35  GATTCTAGGATTCAA 19
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Search completed: December 25, 2002, 12:30:48
Job time : 2991 secs

GenCode version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 14:02:35 ; Search time 54 seconds

67,706 Million cell updates/sec

Title: SCHMIDT875

Partner score: 9

Sequence: 1 ttcnmaaa 9

Scoring table: IDENTITY_MJC

Gap: 10.0, Gapext: 1.0

Search: 364474 seqs: 203117208 residues

Total number of hits satisfying chosen parameters: 221248

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2.6/prodata1/pubmap/US06_PUB.seq;
3: /cgn2.6/prodata1/pubmap/US05_PUB.seq;
4: /cgn2.6/prodata1/pubmap/US04_PUBCOMB.seq;
5: /cgn2.6/prodata1/pubmap/US03_PUBCOMB.seq;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and score derived by analysis of the total score distribution.

SUMMARIES

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1	66.7	9	9	US-10-136-224-13	Sequence 13, Appl
2	66.7	9	9	US-09-842-764-4	Sequence 4, Appl
3	66.7	9	10	US-09-842-764-112	Sequence 12, Appl
4	66.7	9	10	US-09-842-764-112	Sequence 12, Appl
5	66.7	9	10	US-09-842-764-112	Sequence 12, Appl
6	66.7	9	10	US-09-842-764-112	Sequence 12, Appl
7	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
8	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
9	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
10	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
11	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
12	66.7	11	9	US-10-111-877-21	Sequence 21, Appl
13	66.7	12	9	US-10-111-877-23	Sequence 23, Appl
14	66.7	12	9	US-10-111-877-23	Sequence 23, Appl
15	66.7	12	9	US-10-111-877-23	Sequence 23, Appl
16	66.7	12	9	US-10-111-877-23	Sequence 23, Appl
17	66.7	12	9	US-10-111-877-23	Sequence 23, Appl
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ALIGNMENTS

C 20	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 21	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 22	66.7	15	10	US-09-504-231A-935	Sequence 935, App
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C 24	66.7	15	10	US-09-504-231A-935	Sequence 935, App
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C 27	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 28	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 29	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 30	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 31	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 32	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 33	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 34	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 35	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 36	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 37	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 38	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 39	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 40	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 41	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 42	66.7	15	10	US-09-504-231A-935	Sequence 935, App
C 43	66.7	15	10	US-09-504-231A-935	Sequence 935, App
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C 45	66.7	15	10	US-09-504-231A-935	Sequence 935, App

RESULT 1
US-10-136-224-13
Sequence 13, Application US/1016224
GENERAL INFORMATION: 444641
APPLICANT: AGENBANK-CHRISTOPHER J.
APPLICANT: METHOD: SILEMO
TITLE OF INVENTION: SEQUENCES OF CYTOSINE GICRATING
TITLE OF INVENTION: 18 HUMANS
CURRENT FILING DATE: 2002-04-29
PRIORITY FILING DATE: 2002-04-29
PRIORITY APPLICATION NUMBER: US/09/136,224
PRIORITY APPLICATION DATE: 2002-04-29
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTED for Windows version 3.0
LENGTH: 9
TYPE: DNA
FEATURES: MONTE
NAME/KEY: PROMOTER (-461)
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GENERAL INFORMATION:  Jose
SEQUENCE:  US/10113877
APPLICANT:  Bernd Petzold
TITLE OF INVENTION:  DIRECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
TITLE OF INVENTION:  FACTORS
CURRENT APPLICATION NUMBER:  US/09/856,763
PRIORITY DATE:  2001-03-23
CURRENT FILING DATE:  2001-03-23
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
CURRENT APPLICATION NUMBER:  EP 00870057.7
PRIORITY DATE:  2001-03-23
CURRENT FILING DATE:  2001-03-23
NUMBER OF SEQ ID NOS: 150
SOFTWARE:  FASTSD for Windows Version 4.0
LENGTH:  9
TYPE:  DNA
FEATURES:  Artificial Sequence
OTHER INFORMATION:  Consensus sequence for transcriptional factor STAT
NAME/KEY:  also feature
SEQUENCE:  100.0%
OTHER INFORMATION:  n = A.T.C or G
US-09-816-763-112
Query Match
Score 6:  DB 9:  Length 9:
Best Local Similarity 100.0%:  Pred. No. 4,3e+07:
Matches 9:  Conservative 0:  Mismatches 0:  Gaps 0:

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QY 1 TTCNNMMA 9
DB 9 TTCNNMMA 1

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RESULT 7
US-10-113-877-21
Sequence 21: Application US/10113877
Patent No. US62001721B2
GENERAL INFORMATION:
APPLICANT:  Feng, Yu
TITLE OF INVENTION:  Methods of detecting multiple DNA
TITLE OF INVENTION:  Binding protein and DNA interactions in a sample, and
TITLE OF INVENTION:  systems and kits for practicing the same.
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
CURRENT APPLICATION NUMBER:  US/10/113,877
PRIORITY DATE:  2001-03-30
CURRENT FILING DATE:  2001-03-30
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
CURRENT APPLICATION NUMBER:  69/280,658
PRIORITY DATE:  2001-03-30
CURRENT FILING DATE:  2001-03-30
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
PRIOR APPLICATION NUMBER:  69/214,330
PRIORITY DATE:  2001-08-20
PRIOR FILING DATE:  2001-08-20
NUMBER OF SEQ ID NOS: 192
SOFTWARE:  FASTSD for Windows Version 4.0
SEQ ID NO 25
LENGTH:  11
TYPE:  DNA
FEATURES:  Artificial Sequence
OTHER INFORMATION:  oligonucleotide
US-10-113-877-21
Query Match
Score 6:  DB 9:  Length 11:
Best Local Similarity 66.7%:  Pred. No. 2,9e+04:
Matches 6:  Conservative 0:  Mismatches 3:  Indels 0:  Gaps 0:

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QY 1 TTCNNMMA 9
DB 1 TTCNNMMA 9

RESULT 8
US-10-113-877-21/C

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Sequence 21: Application US/10113877
Patent No. US62001721B2
GENERAL INFORMATION:
APPLICANT:  Feng, Yu
TITLE OF INVENTION:  Methods of detecting multiple DNA
TITLE OF INVENTION:  Binding protein and DNA interactions in a sample, and
TITLE OF INVENTION:  systems and kits for practicing the same.
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
CURRENT APPLICATION NUMBER:  US/10/113,877
PRIORITY DATE:  2001-03-30
CURRENT FILING DATE:  2001-03-30
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
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TYPE:  DNA
FEATURES:  Artificial Sequence
OTHER INFORMATION:  oligonucleotide
US-10-113-877-21
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Best Local Similarity 66.7%:  Pred. No. 2,9e+04:
Matches 6:  Conservative 0:  Mismatches 3:  Indels 0:  Gaps 0:

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QY 1 TTCNNMMA 9
DB 9 TTCNNMMA 1

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RESULT 9
US-10-113-877-25
Sequence 25: Application US/10113877
Patent No. US62001721B2
GENERAL INFORMATION:
APPLICANT:  Feng, Yu
TITLE OF INVENTION:  Methods of detecting multiple DNA
TITLE OF INVENTION:  Binding protein and DNA interactions in a sample, and
TITLE OF INVENTION:  systems and kits for practicing the same.
FILE REFERENCE:  CLON-071 (see systems and kits for practicing the same.)
CURRENT APPLICATION NUMBER:  US/10/113,877
PRIORITY DATE:  2001-03-30
CURRENT FILING DATE:  2001-03-30
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PRIORITY DATE:  2001-03-30
PRIOR FILING DATE:  2001-08-20
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SOFTWARE:  FASTSD for Windows Version 4.0
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LENGTH:  11
TYPE:  DNA
FEATURES:  Artificial Sequence
OTHER INFORMATION:  oligonucleotide
US-10-113-877-25
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Score 6:  DB 9:  Length 11:
Best Local Similarity 66.7%:  Pred. No. 2,9e+04:
Matches 6:  Conservative 0:  Mismatches 3:  Indels 0:  Gaps 0:

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QY 1 TTCNNMMA 9
DB 2 TTCNNMMA 10

RESULT 10

schmidt875.rnpb

Sequence 24, Application US/10113877

APPLICANT: Fang, Yu

APPLICANT: Turpin, Pierre
TITLE OF INVENTION: Methods

ATTACHMENT: DEVICES, SYSTEMS AND KITS FOR PRACTICING THE SAME.
FILE REFERENCE: CLON-071

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 60/314,330

SOFTWARE: FASTEST FOR WINDOWS Version 4.0
SPO ID NO 24

TYPE: DNA

FEATURE:

Query Watch 66 28: 2001

QY 1 TTCNNNGAA 9

US-09-504

; FACILE NO. 0520020013458A1
; GENERAL INFORMATION:

APPLICANT: Roberts, Beth

TITLE OF INVENTION: ENZYMATI

FILE REFERENCE: FPI 247/282
CURRENT APPLICATION NUMBER: NS/06/604 333

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1998-04-37

: SEQ ID NO 366

TYPE: RNA

OTHER INFORMATION: Description

Pharynx; Metazo; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
 AUTHORS
 Dunn, D., Aoyagi, A., Babbe, M., Baccotti, T., Dural, B., Hamil, C.,
 Isari, R., Longacre, S., Mahood, M., Nelson, J., Robinson, T., Kelly,
 M., Rose, M., Rose, R., Storer, R., Tinney, A., von Moltkehausen, A.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Contracted (2002) Weiss
 University of Utah
 8112, USA
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 Tel.: 801 585 5606
 Fax: 801 585 5606
 Email: dunn@genetics.utah.edu
 Insert length: 10000 Std error: 0.00
 Plate: 0081 row: 0 column: 05
 Seq primer: CSTRGAMAGACGCGCGT
 High quality sequence stop: 22.
 Class: plasmid ends

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 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="U00C0M035106"
 /clone.lib="Mouse 10kb plasmid U00C1M library"
 /lab.host="E. coli strain XL10-Gold, T1-resistant, p-
 /note="Vector: pMD22v; purified genomic DNA from M.
 Laboratory Mouse DNA Resource obtained from the Jackson
 (http://www.jax.org/resources/documents/dnares/). The DNA
 0.005 ng/ul was amplified by repeated passage through a
 polynucleotide kinase. Adaptor oligonucleotides were
 adapted DNA was purified and size-selected for 2.5 x to
 10.5 kb range using preparative agarose gel.
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (G11721214) (pMD22v). The vector was ligated
 with adaptors complementary to the insert adaptors and
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Pharynx; Metazo; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
 AUTHORS
 Dunn, D., Aoyagi, A., Babbe, M., Baccotti, T., Dural, B., Hamil, C.,
 Isari, R., Longacre, S., Mahood, M., Nelson, J., Robinson, T., Kelly,
 M., Rose, M., Rose, R., Storer, R., Tinney, A., von Moltkehausen, A.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Contracted (2002) Weiss
 University of Utah
 8112, USA
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 Tel.: 801 585 5606
 Fax: 801 585 5606
 Email: dunn@genetics.utah.edu
 Insert length: 10000 Std error: 0.00
 Plate: 0081 row: 0 column: 05
 Seq primer: CSTRGAMAGACGCGCGT
 High quality sequence stop: 22.
 Class: plasmid ends

FEATURES
 source
 1. locus/Qualifiers
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="U00C0M035106"
 /clone.lib="Mouse 10kb plasmid U00C1M library"
 /lab.host="E. coli strain XL10-Gold, T1-resistant, p-
 /note="Vector: pMD22v; purified genomic DNA from M.
 Laboratory Mouse DNA Resource obtained from the Jackson
 (http://www.jax.org/resources/documents/dnares/). The DNA
 0.005 ng/ul was amplified by repeated passage through a
 polynucleotide kinase. Adaptor oligonucleotides were
 adapted DNA was purified and size-selected for 2.5 x to
 10.5 kb range using preparative agarose gel.
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (G11721214) (pMD22v). The vector was ligated
 with adaptors complementary to the insert adaptors and
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

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 Best Local Similarity 66.7% Pred. No. 4:6+05:
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 DB 15 TTTCCNCA 7

RESULT 13
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 DEFINITION 2K085C01F Mouse 10kb plasmid U00C1M library Mus musculus genomic
 accession A281674.1 GI:1298482
 VERSION A281674.1 GI:1298482
 KEYWORDS house mouse;
 ORIGIN Mus musculus

BASE COUNT
 ORIGIN
 Query Match 66.7% Score 6: DB 17: Length 22:
 Best Local Similarity 66.7% Pred. No. 4:6+05:
 Matches 6: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
 Oy 1 111 111
 3 TTTCCNCA 11

RESULT 14
 LOCUS A281674 22 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2K085C01F Mouse 10kb plasmid U00C1M library Mus musculus genomic
 accession A281674.1 GI:1298482
 VERSION A281674.1 GI:1298482
 KEYWORDS house mouse;
 ORIGIN Mus musculus

